

TECHNICAL BULLETIN



ENHANCEMENTS TO ANGUS BREEDPLAN

DECEMBER 2017

A number of enhancements have been implemented in the December 2017 Angus BREEDPLAN analysis.

These enhancements are part of the ongoing maintenance and improvement to the Angus BREEDPLAN genetic evaluation, and will result in the calculation of EBVs that better predict the genetic merit of Australian Angus animals.

Calculation of EBVs for North American Animals

Angus BREEDPLAN incorporates EPDs for American Black and Red Angus, Canadian Black and Red Angus, and American Brangus animals in order to improve the calculation of EBVs for North American genetics that have been imported into Australia.

Several enhancements have been implemented with regards to the calculation of EBVs for North American animals:

- As a result of considerable analytical changes being made to the genetic evaluations in which the EPDs are calculated, particularly the genetic evaluation conducted by the American Angus Association, the Animal Genetics & Breeding Unit (AGBU) has reviewed and updated the parameters that are utilised when incorporating the North American EPDs into the calculation of Angus BREEDPLAN EBVs.
- The EPDs for all imported American and Canadian Black and Red Angus animals has been updated to ensure the most up-to-date EPDs are utilised.
- EPD information has been incorporated on a greater number of animals recorded with the American Angus Association.

In addition, arrangements have been made to enable the EPD information to be updated on a more regular basis, with updated EBVs now to be incorporated in the March, June, August and December analyses each year. Previously EPDs were updated in the June and December analyses.

The enhancements, plus the more regular updating of EPD information, will result in the calculation of EBVs that better predict the breeding value of North American animals within Angus BREEDPLAN.

Implementation of Single Step Analytical Software

A new approach for incorporating genomic information

into the calculation of EBVs within Angus BREEDPLAN has been implemented for traits within the main multi-trait analysis.

Referred to as “single step analytical software”, the new approach simultaneously utilises genomic, pedigree and performance information, placing appropriate emphasis on all available sources of information, to generate the best possible prediction of an animal’s breeding value.

The new single step analytical approach will more optimally utilise genomic information within Angus BREEDPLAN, resulting in the calculation of EBVs that better predict the breeding value of Angus animals.

Note: The new analytical model does not apply to the calculation of EBVs for Calving Ease Direct, Calving Ease Daughters, Docility, and the five Structural Soundness EBVs. Further work is required to utilise the single-step approach for these non-linear traits.

Changes to Genomic Information Included in Angus BREEDPLAN

In association with the implementation of the single step analytical software, the genomic predictions previously incorporated into the main multi-trait component of the Angus BREEDPLAN analysis (i.e. GeneSeek MBVs, Zoetis MVPs, Beef CRC DGVs) have been replaced by raw genotype (SNP) information.

Additionally, the raw genomic information is now subjected to new, stringent quality assurance standards before it is deemed eligible for inclusion in Angus BREEDPLAN.

These two factors have resulted in changes to the information that is analysed for some animals.

Specifically:

- Genomic information may now be incorporated into the calculation of the EBVs for some animals that previously did not have genomic information analysed (~4000 animals).
- Genomic information may no longer be incorporated into the calculation of the EBVs for some animals that previously had genomic information analysed (~2000 animals).
- Cross checking of an animal’s genomic information with the details recorded for the respective animal on

the Angus Australia database has resulted in corrections to the pedigree, gender or breed of some animals (~200 animals).

Angus Australia members can determine if genomic information has been utilised in the calculation of EBVs for their animals by referring to the “traits observed” section that is displayed underneath an animal’s EBVs on the Angus Australia Database Search facility. A label of “Genomics” will display for animals when genomic information has been incorporated into the calculation of their EBVs.

Changes to EBVs

The enhancements that have been implemented, along with the associated changes to the genomic information that is analysed for some animals, have resulted in considerable changes to the EBVs, selection indexes and EBV accuracies that are calculated for animals within the December 2017 Angus BREEDPLAN analysis, particularly those with genomic information.

Importantly, the new EBVs provide a better estimate of each animal’s breeding value, and will better facilitate the identification of Angus genetics that are most aligned with the breeding objective in Angus breeding programs.

Additional Changes

Work continues to collate any additional genomic information that is available for Angus animals, and to resolve a small number of quality assurance concerns that have been highlighted with the genomic information of some animals. Future changes to the EBVs of some animals are expected over coming months as this work progresses.

Further Information

To further discuss any of the enhancements that have been implemented in the December 2017 Angus BREEDPLAN analysis, please contact:

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UNDERSTANDING SINGLE STEP ANALYTICAL SOFTWARE

Genomics, the term given to describe a range of DNA based technologies concerned with the structure, function, evolution, and mapping of genomes, is a science receiving much interest around the world among breeders of all livestock species.

The Angus breed has led the Australian beef industry with the application of genomics, with genomic information being incorporated into the Angus BREEDPLAN genetic evaluation since April 2011. Since this time, genomics has been increasingly adopted by Angus breeders in Australia, with genomic information now analysed in Angus BREEDPLAN for over 30,000 animals.

Although the inclusion of genomic information in Angus BREEDPLAN has become mainstream, genomics is still very much an evolving science.

The December 2017 Angus BREEDPLAN analysis heralded a new era for the utilisation of genomics by Australian Angus breeders with the implementation of a new and improved approach for incorporating genomic information into the calculation of EBVs.

Referred to as “single step analytical software”, the implementation of the new software is a result of collaborative research and development over recent years between the Animal Genetics & Breeding Unit (AGBU), the Agricultural Business Research Institute (ABRI), Angus Australia, and the New Zealand Angus Association, with funding assistance from Meat & Livestock Australia (MLA).

Similar single step analytical software models have either recently been implemented, or are in the process of being implemented into all major animal breeding genetic evaluations around the world.

Previous Procedure for Incorporation of Genomic Information

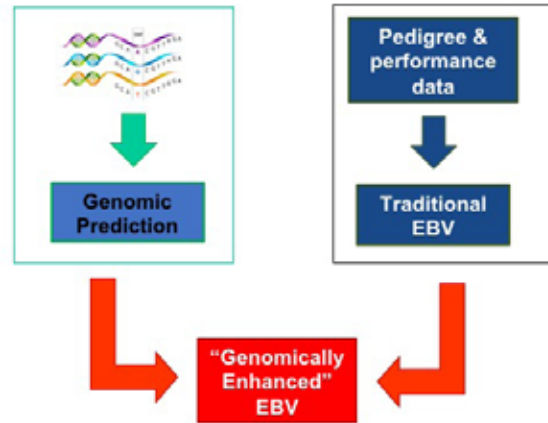
The procedure traditionally used for the incorporation of genomic information into Angus BREEDPLAN used a multi-step process.

Step 1 involved using the genomic data for an animal to generate a genomic prediction of the animal's breeding value. This is often referred to as a Molecular Breeding Value (MBV) or Molecular Value Prediction (MVP).

Step 2 involved using the pedigree and performance information for an animal (and its relatives) to calculate a traditional EBV (i.e. estimated breeding value) for the animal.

Step 3 combined the animal's genomic prediction with its traditional EBV, to generate a genomically enhanced EBV. This process of combining the genomic prediction and traditional EBV is referred to as “blending”.

Figure 1 : Previous Multi-Step Analytical Approach

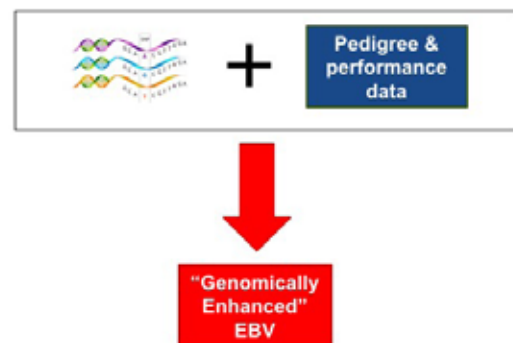


While the multi-step analytical model represented the most sophisticated approach available at the time, different methodologies that use genomics in a more effective and appropriate manner have since been developed.

New Single Step Analytical Model

The new single step analytical model simultaneously utilises genomic, pedigree and performance information, placing appropriate emphasis on all available sources of information, to generate the best possible estimate of an animal's breeding value.

Figure 2 : New Single Step Analytical Approach



Benefits of Single Step Analytical Model

The main benefit of the new analytical approach is how genetic relationships between animals are determined.

With a traditional pedigree based approach, the relationships between animals within Angus BREEDPLAN are determined by pedigree alone. For example, pedigree

would predict that the genetic relationship between full siblings (i.e. animals with the same sire and dam) is 0.5, meaning full siblings are predicted to have 50% of genes in common when calculating traditional pedigree-based breeding values.

Understanding the way that DNA is inherited, it is known that there will in fact be variation between these relationships, and the true genetic relationship between full siblings is likely to range between 0.4 – 0.6.

Similarly, pedigree may predict that two animals are unrelated, but in reality, the animals may share common genes, and have a genetic relationship greater than 0.

The new single step approach improves the precision in which EBVs are calculated by better quantifying genetic relationships, using both genomic (where available) and pedigree information to determine the genetic relationships between animals.

Other Benefits

In addition to better determining the genetic relationship between animals, the single step analytical approach has a number of additional benefits, including:

- Any errors in the pedigree of animals are routinely overcome (providing both the animal and its parent/s have genomic information available).
- Genomic information contributes to not only the EBVs of the animal that has been genotyped, but also contributes to the EBVs for the animal's relatives (e.g. parents, progeny).
- Genomic information now contributes to all EBVs that are calculated within the main multi-trait analysis within Angus BREEDPLAN, rather than being limited to a sub set of traits. The main multi-trait component of the Angus BREEDPLAN analysis includes the calculation of EBVs for all traits except Calving Ease Direct, Calving Ease Daughters, Docility, and the five Structural Soundness EBVs.
- Genomic effects are now updated each time that an Angus BREEDPLAN analysis is conducted, ensuring the most up-to-date genomic effects are utilised when calculating EBVs. The need to regularly re-calibrate the prediction equations that are used to calculate genomic predictions has also been removed.
- Genomic information is now given different (and more appropriate) emphasis when calculating the EBVs for each animal, based on each individual animal's genetic relationship to the reference population (being animals with both genomic and performance information).

The net result is that the new single step analytical approach now more optimally utilises genomic information within the main multi-trait component of the Angus BREEDPLAN analysis, and provides Angus breeders in Australia and New Zealand with EBVs that are the best possible estimate of an animal's breeding value.

Which EBVs are calculated using the Single Step Approach?

The new single step analytical software has been implemented into the main multi-trait component of the Angus BREEDPLAN analysis, meaning that several different methodologies are now utilised when incorporating genomic information into Angus BREEDPLAN, subject to the EBV being calculated (see Table 1).

Further research is now underway to enable the single-step approach to be used for the calculation of EBVs for the calving ease, docility and structural soundness traits.

TABLE 1: ANALYTICAL METHODOLOGY USED WHEN CALCULATING EACH EBV IN ANGUS BREEDPLAN

Trait	Methodology
Calving Ease Direct	Multi-step (blending)
Calving Ease Daughters	Multi-step (blending)
Birth Weight	Single step
Gestation Length	Single step
200 Day Growth	Single step
400 Day Weight	Single step
600 Day Weight	Single step
Mature Cow Weight	Single step
Milk	Single step
Scrotal Size	Single step
Days to Calving	Single step
Carcase Weight	Single step
Carcase EMA	Single step
Carcase Rib Fat	Single step
Carcase Rump Fat	Single step
Retail Beef Yield	Single step
Carcase IMF	Single step
NFI-p	Single step
NFI-f	Single step
Docility	No genomic information incorporated
Front Foot Angle	No genomic information incorporated
Front Foot Claw Set	No genomic information incorporated
Rear Foot Angle	No genomic information incorporated
Rear Leg Hind View	No genomic information incorporated
Rear Leg Side View	No genomic information incorporated

How Much Did EBVs Change?

The EBVs for some animals have changed considerably with the implementation of the single step software, particularly for animals that have genomic information available. Likewise, the accuracy values published with the EBVs for some animals have changed.

Importantly, the EBVs and EBV accuracies that are calculated by the new single step analytical software provide a better prediction of each animal's breeding value, and have improved the genetic evaluation that is available to Angus breeders in Australia and New Zealand.

For the statistically minded, Table 2 details the correlation, or relationship, between the EBVs derived using the new single step analytical software versus the EBVs derived using the previous multi-step blending approach for animals that have genomic information analysed in Angus BREEDPLAN. The correlation is reflective of the amount in which the EBVs for animals have re-ranked with the implementation of the new single step analytical software.

This information is also provided graphically for 400 Day Weight, IMF and Angus Breeding Index in Figures 3, 4, 5, 6, 7 & 8.

Table 2: Correlation between the EBVs derived using the new single step analytical software versus the EBVs derived using the previous two step blending approach (for animals with genomic information)

	Sires	Non-Parent Males
No. of Animals	2241	9122
CED	1.00	1.00
CEDtrs	1.00	1.00
BW	0.95	0.90
GL	0.95	0.90
200	0.95	0.89
400	0.95	0.90
600	0.95	0.90
MCW	0.93	0.87
Milk	0.91	0.87
SC	0.92	0.88
DTC	0.91	0.87
CW	0.95	0.89
EMA	0.92	0.88
Rib	0.92	0.86
Rump	0.92	0.86
RBV	0.91	0.85
IMF	0.95	0.93
NFI-P	0.90	0.86
NFI-F	0.88	0.82
Doc	1.00	1.00
ABI	0.96	0.94
DOM	0.96	0.93
HGN	0.96	0.94
HGS	0.96	0.93

Figure 3 - Sires - 400 Day Weight

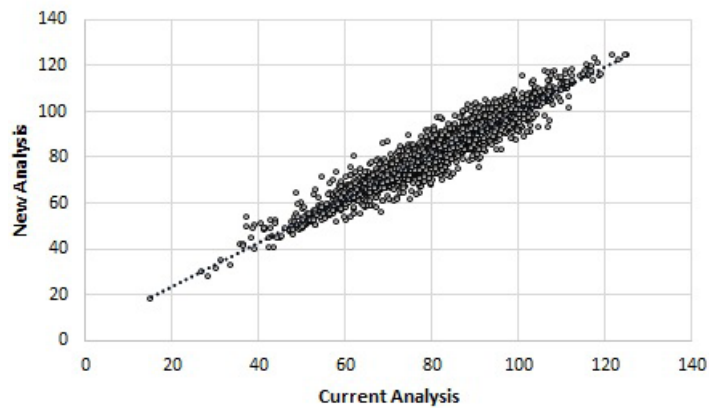


Figure 4 - Non Parent Bulls - 400 Day Weight

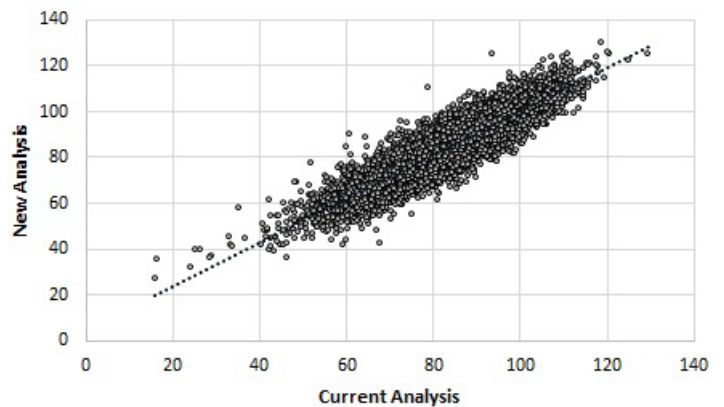


Figure 5 - Sires - Carcase IMF

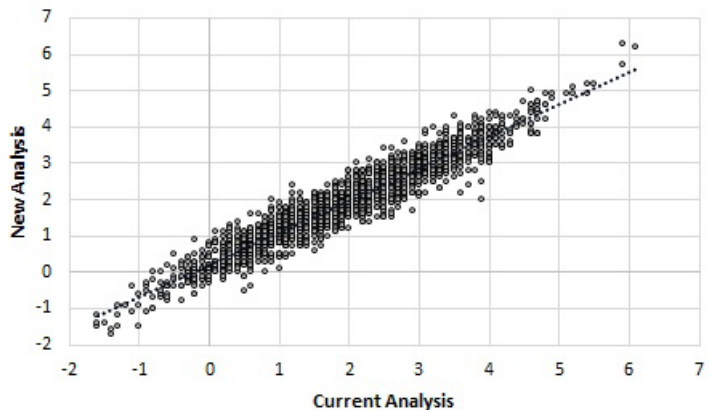


Figure 6 - Non Parent Bulls - Carcase IMF

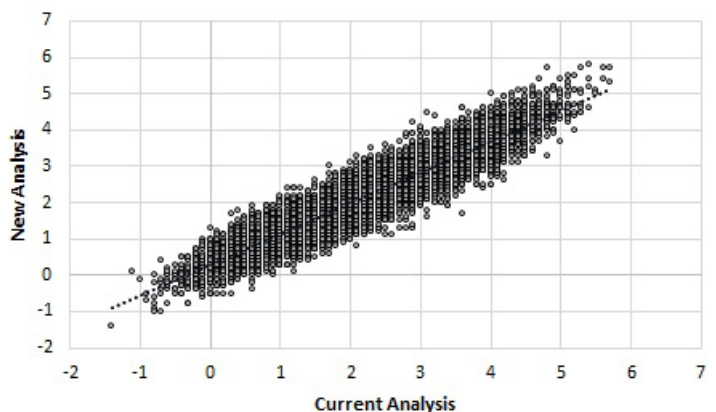


Figure 7 - Sires - Angus Breeding Index

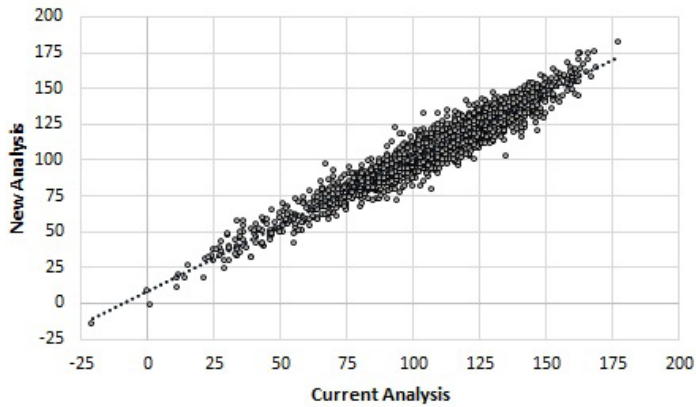
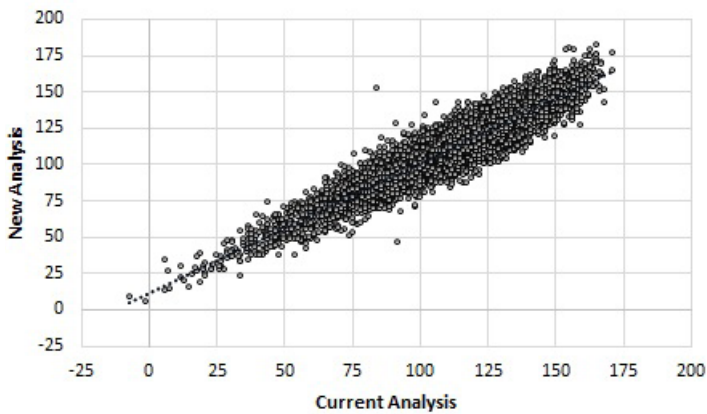


Figure 8 - Non Parent Bulls - Angus Breeding Index



What Does Single Step Analytical Software Mean for Angus Breeders?

Other than changes to EBVs and EBV accuracy values for some animals, there will be little noticeable change to

Angus breeders with the implementation of the new single step analytical software.

The range of DNA services that are available to Angus Australia members, and the cost of those DNA services remains unchanged. Likewise, the manner in which DNA samples need to be collected and submitted to Angus Australia remains unchanged, as is the manner in which DNA samples are handled at the DNA laboratory.

The main implication is that genomic information is now utilised more optimally within the Angus BREEDPLAN analysis, and an improved genetic evaluation service is available to Angus breeders in Australia and New Zealand.

The implementation of single step analysis will however mean that traditional EBVs, and genomic predictions are no longer produced, and so Molecular Value Predictions (MVPs) will not be provided by Zoetis for i50K or HD50K tests ordered through Angus Australia after December 1st.

Further Information

To further discuss the incorporation of genomic information in Angus BREEDPLAN, including the new single step analytical software, please contact:

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